

SEQUENCE LISTING

<110> Hartley, James L.

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Temple, Gary F.

Cheo, David

<120> Compositions and Methods for Use in Recombinational Cloning of Nucleic Acids

<130> 0942.4680003

<140> 09/517,466

<141> 2000-03-02

<150> US 60/122,389

<151> 1999-03-02

<150> US 60/126,049

<151> 1999-03-23

<150> US 60/136,744

<151> 1999-05-28

<160> 285

<170> PatentIn version 3.1

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ttttacgttt ctcgttcagc tttttgtac aaagttggca ttataaaaaaa gcattgctca 180
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gaaagctggg tn 12

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<223> attB1 fused into a His6 fusion vector

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20 25 30

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cagacggcat gatgaacctg aa

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<210> 63

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<210> 77

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<212> DNA

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<223> 'n' can be any nucleotide (A, T, C, G or U)

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<223> 'n' can be any nucleotide (A, T, C, G or U)

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<223> attB2.10 Amplification Site

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<223> attB1n16-20 PCR Primer

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<223> 'n' can be any nucleotide (A, T, C, G or U)

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<222> (321) .. (626)

<223> ccdB

<220>

<221> gene

<222> (655) .. (754)

<223> attL2

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<222> (877) .. (1686)

<223> KmR

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<221> gene

<222> (1791) .. (2364)

<223> ori

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<222> (656)..(755)

<223> attL2

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<222> (878)..(1687)

<223> KmR

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<222> (1792)..(2365)

<223> ori

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<222> (883)..(1692)
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<222> (1797)..(2370)
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<223> ori

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<222> (673)..(772)

<223> attL2

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<222> (1809)..(2382)

<223> ori

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<222> (904)..(1713)

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<222> (1818)..(2391)

<223> ori

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ANSWER The total amount of money spent on the two items is \$180.

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Ile Arg Tyr Arg Ile
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48

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<223>

<400> 215

ttg tac aaa aaa gca ggc ttc gaa cta agg aaa tac tta cat atg gga
Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1 5 10 15

48

acc aat tca gtc gac tgg atc cg^g tac cga att cgc
Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

84

<210> 216

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 216

Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1 5 10 15

Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 217

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 217
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<210> 218

<211> 88

<212> DNA

<213> Artificial Sequence

<220>

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<220>

<221> CDS

<222> (1)...(87)

<223>

<400> 218
ttg tac aaa aaa gca ggc ttc gaa gga gat aga acc aat tct cta agg 48
Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

aaa tac tta acc atg gtc gac tgg atc cgg tac cga att c 88
Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 219

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 219

Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 220

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (2) .. (49)

<223>

<400> 220

g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa
Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

g

49

50

<210> 221

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 221

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

<210> 222

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST1

<400> 222

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aatttcacac aggaaacaga caggtataagg atcacaagtt tgtacaaaaa agctgaacga 120

<210> 223

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST2

<220>

<221> CDS

<222> (94)..(135)

<223>

<400> 223

aatattctga aatgagctgt tgacaattaa tcatccggtc cgtataatct gtggaattgt 60
gagcggataa caatttcaca caggaaacag acc atg tcg tac tac cat cac cat 114
Met Ser Tyr Tyr His His His His
1 5

cac cat cac ggc atc aca agt ttgtacaaaa aagctgaa 153
His His His Gly Ile Thr Ser
10

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST2

<400> 224

Met Ser Tyr Tyr His His His His His Gly Ile Thr Ser
1 5 10

<210> 225

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST3

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 225
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gtggaattgt gagccgataa caatttcaca caggaaacag tattc atg tcc cct ata
Met Ser Pro Ile 117
1
cta ggttattgga aaattaaggg ctttgtaaa ccc
Leu 153
5

<210> 226

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST3

<400> 226

Met Ser Pro Ile Leu
1 5

<210> 227
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
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<222> (10)..(63)
<223>

<400> 227
ctggttccg cgt gga tct cgt cgt gca tct gtt gga tcc cca tca aca agt 51
Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser
1 5 10

ttg tac aaa aaa gctgaacgag aaacgtaaaa tgatataaat atcaatata 102
Leu Tyr Lys Lys
15

<210> 228
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST3
<400> 228

Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser Leu Tyr
1 5 10 15

Lys Lys

<210> 229
<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST4

<220>

<221> CDS

<222> (97) .. (246)

<223>

<400> 229

gcaaataattc tgaaatgagc tgttgacaat taatcatccg gtccgtataa tctgtggaat 60
tgtgagcgga taacaatttc acacaggaaa cagacc atg ggt cat cat cat cat 114
Met Gly His His His His
1 5

cat cac gat tac gat atc cca acg acc gaa aac ctg tat ttt cag ggc 162
His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn Leu Tyr Phe Gln Gly
10 15 20

gcc cat atg agc gat aaa att att cac ctg act gac gac agt gat gac 210
Ala His Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Asp Asp
25 30 35

gat gac aag gta ccc atc aca agt ttg tac aaa aaa gctgaacga 255
Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr Lys Lys
40 45 50

<210> 230

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST4

<400> 230

Met Gly His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu 15
1 5 10 15

Asn Leu Tyr Phe Gln Gly Ala His Met Ser Asp Lys Ile Ile His Leu
20 25 30

Thr Asp Asp Ser Asp Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr
35 40 45

Lys Lys
50

<210> 231
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST5
<400> 231
aggcacccca ggctttacac tttatgcttc cggctcgat gttgtgtgga attgtgagcg 60
gataacaatt tcacacagga aacagctatg accatgatta cgccaagctc taatacgact 120
cactataggg aaagctggta cgcctgcagg taccggtccg gaattcccg gtcgacgatc 180
acaagtttgt acaaaaaagc tgaa 204

<210> 232
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST5
<400> 232
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agaggatcca agcttacgta cgcgtgcata cgacgtcata gctcttctat agtgtcacct 120
aaattcaatt cactggccgt cgtttacaa cgtcgtgact gggaaaaccc tggcgttacc 180
caacttaatc gccttgcagc acat 204

<210> 233
<211> 204
<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 233
taacgccagg gtttcccag tcacgacgtt gtaaaacgac ggccagtgaa ttgaatttag 60
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagcttg gatcctctag 120
agcggccgccc gactagtgtat cacaagtttg tacaaaaaaag ctgaacgaga aacgtaaaat 180
gatataaata tcaatatattt aaat 204

<210> 234

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 234
tatttatatac atttacgtt tctcggttcag ctttcttgta caaagtggtg atcggtcgacc 60
cggttattcc ggaccgggtac ctgcaggcgt accagcttc cctatagtga gtcgtatttag 120
agcttggcgt aatcatggtc atagctgttt cctgtgtgaa attgttatcc gctcacaatt 180
ccacacaaca tacgagccgg aagcataaaag tgtaaaggctt ggggtgccta atgagtgagc 240
taactcacat taatt 255

<210> 235

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST7

<400> 235
ccattgacgc aaatggggcgg taggcgtgtt cgggtggagg tctatataag cagagcttgt 60
tttagtgaacc gtcagatcgcc ctggagacgc catccacgct gttttgacctt ccatagaaga 120

caccgggacc gatccagcct ccggactcta gcctaggccg cgagcgat aacaattca	180
cacagggaaac agctatgacc actaggctt tgcaaaaagg tathtaggt acactataga	240
aggtacgcct gcaggtaccg gtccggaatt cccatcacaa gtttgtacaa aaaagctgaa	300
cgagaa	306

<210> 236

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST8

<400> 236

cgtatactcc ggaatattaa tagatcatgg agataattaa aatgataacc atctcgcaa	60
taaataagta ttttactgtt ttcgtaacag ttttgaata aaaaaaccta taaatattcc	120
ggattattca taccgtcccc caatcgcccg cggatcatca caagttgtt caaaaaagct	180
gaacgagaaa cgtaaaatga tata	204

<210> 237

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST9

<400> 237

ttggcgaggg acattaaggc gtttaagaaa ttgagaggac ctgttataca cctctacggc	60
ggtccttagat tggtgcgatatacacaat ttctgattgg atcccggtcc gaagcgccgt	120
tcccatcaa caagttgtt caaaaaagct gaa	153

<210> 238

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST10

<220>

<221> CDS

<222> (109)..(201)

<223>

<400> 238

aaataagtat tttactgttt tcgtaacagt tttgtataaa aaaaacctat aaatattccg 60

gattatttcat accgtccccac catcgggcgc gatatctcggt ccgaaacc atg tcg tac 117
Met Ser Tyr
1

tac cat cac cat cac cat cac gat tac gat atc cca acg acc gaa aac 165
Tyr His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn
5 10 15

ctg tat ttt cag ggc atc aca agt ttg tac aaa aaa gct 204
Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 239

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST10

<400> 239

Met Ser Tyr Tyr His His His His His Asp Tyr Asp Ile Pro Thr 15
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 240

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST11

<400> 240
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accggggaccg atccaggcctc cgccggcccg aattcgagct cggtacccgg ggatcctcta 120
gagtcgaggt cgacggtatac gataagcttg atatcaacaa gtttgtacaa aaaagctgaa 180
cgagaaaacgt aaaatgatat aaat 204

<210> 241

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST12.2

<400> 241
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accgatccag cctccggact ctagcctagg ccgcggagcg gataacaatt tcacacagga 120
aacagctatg accatttaggc ctggcaaaa agctattttag gtgacactat agaaggtacg 180
cctgcaggta ccggccggaa attcccatca acaagttgt acaaaaaagc tgaacgagaa 240
acgtaaaaatg atata 255

<210> 242

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST13

<400> 242
tgggcaaacc aagacagcta aagatctctc acctacccaa caatcccccc ctgaaaaaaaa 60
taaattcata taaaaaacat acagataacc atctgcggtg ataaattatc tctggcggtg 120

ttgacataaa taccactggc ggtgatactg agcacatcg caggacgcac tgaccaccat 180
gaaggtgacg ctctaaaaa ttaagccctg aagaaggca gcattcaaag cagaaggctt 240
tgggtgtgt gatacgaaac gaagcattgg gatcatcaca agtttgtaca aaaaagctga 300

<210> 243

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST14

<400> 243

tgcggccac gatgcgtccg gcgttagagga tcgagatctc gatccgcga aattaatacg 60
actcactata gggagaccac aacggttcc ctctagatca caagttgtca caaaaaagct 120

<210> 244

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> 'n' can be any nucleotide (A, T, C, G or U)

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 244

natcgagatc tcgatccgc gaaattaata cgactcacta tagggagacc acaacggttt 60
ccctctagaa ataattttgt ttaactttaa gaaggagata tacat atg tcc cct ata 117
Met Ser Pro Ile
1

cta ggttattgga aaattaaggg ccttgtcaa cccactcgac ttcttttggaa 170
Leu
5

atatcttgaa gaaaaatatg aagagcattt gtat 204

<210> 245

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> may be any nucleotide

<400> 245

Met Ser Pro Ile Leu
1 5

<210> 246

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

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<221> CDS

<222> (70)..(99)

<223>

<400> 246
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cgtccatgg tcg aat caa aca agt ttg tac aaa aaa gct gaacgagaaa 109
Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

cgtaaaatga tataaatatc aatatattaa attagatttt gcat 153

<210> 247

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<400> 247
Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 248

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (100)..(111)

<223>

<400> 248
gatctcgatc ccgcgaaatt aatacgactc actataggga gaccacaacg gtttccctct 60
agaaaataatt ttgtttaact ttaagaagga gatatacat atg agc gat aaa 111
Met Ser Asp Lys
1

attattcacc tgactgacga cagtttgac acggatgtac tc 153

<210> 249

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 249

Met Ser Asp Lys
1

<210> 250

<211> 153

<212> DNA

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<220>

<223> pDEST16 multiple cloning site

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<221> CDS

<222> (82)..(123)

<223>

<400> 250

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aacctggcccg gttctggttc t ggt gat gac gat gac aag atc aca agt ttg 111
Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu
1 5 10

tac aaa aaa gct gaacgagaaaa cgtaaaaatga tataaatatc 153
Tyr Lys Lys Ala

<210> 251

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 251

Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 252

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<220>

<221> CDS

<222> (94)..(153)

<223>

<400> 252

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aattttgtttaaacttaagaaggagatatacatatgttcgtac tac cat cac cat 114
Met Ser Tyr Tyr His His His
1 5

cac cat cac ctc gaa tca aca agt ttg tac aaa aaa gct 153
His His His Leu Glu Ser Thr Ser Leu Tyr Lys Lys Ala
10 15 20

<210> 253

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<400> 253

Met Ser Tyr Tyr His His His His His Leu Glu Ser Thr Ser Leu
1 5 10 15

Tyr Lys Lys Ala
20

<210> 254

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST18 p10 Promoter

<400> 254

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tcctcggttt tctggaaggc gagcatcggtt tgttcgccca ggactctagc tatagttcta 120
gtggttggct acgtatcgag caagaaaata aaacgccaaa cgcgttggag tcttgtgtgc 180
tatTTTaca aagattcaga aatacgcac tattacaaca agggggacta tgaattatg 240
cattttgagg atgcgggac cttaattca acccaacaca atatattata gttaaataag 300
aattatTTat caaatcattt gtatattaat taaaatacta tactgtaaat tacatTTat 360
ttacaatgag gatcatcaca agttgtaca aaaaagctga acgagaaacg taaaatgata 420

<210> 255

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST19 39K Promoter

<400> 255

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aaaaaaacgg ccagtttctt ccacaaactc ggcacggct gtctcgtaaa cttttcggtc 120

gcaacaatcg cgatgaccc tcgttatgg aatttttct aaaaaagtgt cttcatgtc 180
ggcgccggcg ttcgcgtcc ggtacgcgcg acggcacac agcaggacag cttgtccgg 240
ctcgattatc ataaacaatc ctgcaggcat gcaagctgga tcatacacaag ttgtacaaa 300

<210> 256

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (163)..(174)

<223>

<400> 256
ggctacgtat actccgaa attaatagat catggagata attaaaatga taaccatctc 60
gcaaataaat aagtattta ctgtttcgt aacagtttg taataaaaaa acctataaat 120
attccggatt attcataaccg tcccaccatc gggcgccgat cc atg gcc cct ata 174
Met Ala Pro Ile
1
ctaggttatt ggaaaattaa gggccttgt 204

<210> 257

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<400> 257

Met Ala Pro Ile

1

<210> 258
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST20 Polyhedron Promoter
<220>
<221> CDS
<222> (1)..(48)
<223>

<400> 258
tcg gat ctg gtt ccg cgt cat aat caa aca agt ttg tac aaa aaa gct
Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10 15

48

gaacgagaaa cgtaaaatga tataaatatc aatatattaa attagat 95

<210> 259
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST20 Polyhedron Promoter
<400> 259

Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10 15

<210> 260
<211> 204
<212> DNA
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<220>

<223> pDEST21 Promoter region

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<221> CDS

<222> (163)..(180)

<223>

<400> 260
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attgttctcg ttccctttct tccttgtttc ttttctgca caatatttca agctatacca 120
agcataacaat caactccaag cttgaagcaa gcctcctgaa ag atg aag cta ctg 174
Met Lys Leu Leu
1

tct tct atcgaacaag catgcgatat ttgc 204
Ser Ser
5

<210> 261

<211> 6

<212> PRT

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<223> pDEST21 Promoter region

<400> 261
Met Lys Leu Leu Ser Ser
1 5

<210> 262

<211> 102

<212> DNA

<213> Artificial Sequence

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<223> pDEST21 Promoter region

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<221> CDS

<222> (37) .. (78)

<223>

<400> 262

gaagagagta gtaacaaagg tcaaagacag ttgact gta tcg tcg agg tcg aat
Val Ser Ser Arg Ser Asn
1 5

54

caa aca agt ttg tac aaa aaa gct gaacgagaaa cgtaaaatga tata
Gln Thr Ser Leu Tyr Lys Lys Ala
10

102

<210> 263

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> pDEST21 Promoter region

<400> 263

Val Ser Ser Arg Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 264

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST22 Promoter region

<220>

<221> CDS

<222> (217) .. (228)

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<400> 264
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aaataaaaaaa agtttgcgc tttgctatca agtataaata gacctgcaat tattaatctt 120
ttgtttccctc gtcattgttc tcgttccctt tcttccttgc ttcttttct gcacaatatt 180
tcaagctata ccaaggatac aatcaactcc aagctt atg ccc aag aag 228
Met Pro Lys Lys
1
aagcggagg tctcgagcg cgccaat 255

<210> 265

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST22 Promoter region

<400> 265
Met Pro Lys Lys
1

<210> 266

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST22

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<221> CDS

<222> (28) .. (66)

<223>

<400> 266
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Glu Gly Gly Ser Asn Gln Thr Ser Leu

1

5

tac aaa aaa gct gaacgagaaaa cgtaaa 82
Tyr Lys Lys Ala
10

<210> 267

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST22

<400> 267

Glu Gly Gly Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 268

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 268

atcccgcgaa attaatacga ctcactatag ggagaccaca acggtttccc tctagatcac 60

aagtttgtac aaaaaagctg aacgagaaaac gtaaaaatgat at 102

<210> 269

<211> 153

<212> DNA

<213> Artificial Sequence

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<223> pDEST23 T7 promoter

<220>

<221> CDS

<222> (61)..(126)

<223>

<400> 269

ttttatgca aaatctaatt taatatattg atatttat catttacgt ttctcggtca 60

gct ttc ttg tac aaa gtg gtg att atg tcg tac tac cat cac cat cac 108
Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1 5 10 15

cat cac ctc gat gag caa taactagcat aacccttgg ggccctct 153
His His Leu Asp Glu Gln
20

<210> 270

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 270

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
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His His Leu Asp Glu Gln
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<210> 271

<211> 102

<212> DNA

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<220>

<223> pDEST24 T7 promoter

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cctcttagatc acaagtttgt acaaaaaagc tgaacgagaa ac 102

<210> 272
<211> 102
<212> DNA
<213> Artificial Sequence

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<221> CDS
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<400> 272
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          Ala Phe Leu Tyr Lys Val Val Ile Met Ser
          1           5           10

cct ata cta ggTTATTGGA aaATTAAGGG CCTTGTGCAA CCCACTCGAC tt
Pró Ile Leu                                         102

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<210> 273
<211> 13
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<220>
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<400> 273

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Pro Ile Leu
1 5 10

<210> 274
<211> 102
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<223> 'n' can be any nucleotide (A, T, C, G or U)

<400> 274
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ctagatcaca agtttgtaca aaaaagctga acgagaaaacg ta 102

<210> 275
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<212> DNA
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<221> CDS
<222> (19)..(60)
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<400> 275
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Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp
1 5 10
aaa att att cacctgactg acgacagttt tgacacggat gtactcaaag cg 102
Lys Ile Ile

<210> 276
<211> 14
<212> PRT

<213> Artificial Sequence

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<223> pDEST25 T7 promoter

<400> 276

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp Lys Ile Ile
1 5 10

<210> 277

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<220>

<221> CDS

<222> (238)..(297)

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<400> 277

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acaactccgc cccattgacg caaatggcg gttaggcgtgt acgggtggag gtcttatataa 120

gcagagctcg tttagtgaac cgtcagatcg cctggagacg ccatccacgc tgtttgacc 180

tccatagaag acaccggac cgatccagcc tccggactct agcctaggcc gcggacc 237

atg gcg tac tac cat cac cat cac tct aga tca aca agt ttg 285
Met Ala Tyr Tyr His His His His His Ser Arg Ser Thr Ser Leu

1 5 10 15

tac aaa aaa gct gaacgagaa 306

Tyr Lys Lys Ala
20

<210> 278

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

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<400> 278

Met Ala Tyr Tyr His His His His His Ser Arg Ser Thr Ser Leu
1 5 10 15

Tyr Lys Lys Ala
20

<210> 279

<211> 255

<212> DNA

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<220>

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<400> 279

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gccatccacg ctgtttgac ctccatagaa gacaccggga ccgatccagc ctccggactc 120

tagccttaggc cgccggacc atg gcc cct ata cta ggttattgga aaattaagg 173

Met Ala Pro Ile Leu

1

5

ccttgtgcaa cccactcgac ttctttgga atatcttgaa gaaaaatatg aagagcattt 233

gtatgagcgc gatgaaggatg at 255

<210> 280

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<212> PRT

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<400> 280

Met Ala Pro Ile Leu
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<210> 281

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

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<222> (37)..(75)

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<400> 281

tttgggtggtg gcgaccatcc tccaaaatcg gatctg gtt ccg cgt tct aga tca
Val Pro Arg Ser Arg Ser
1 5

aca agt ttg tac aaa aaa gct gaacgagaaaa cg
Thr Ser Leu Tyr Lys Lys Ala

54

87

10

<210> 282
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> pDEST27 promoter
<400> 282

Val Pro Arg Ser Arg Ser Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 283
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<212> DNA
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<223> pEXP501

<400> 283
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acaatttcac acaggaaaca gctatgacca ttaggcctat ttaggtgaca ctatagaaca 180
agtttgtaca aaaaagcagg ctggtaccgg tccggaaattc ccgggatatac gtcgacgagc 240
tcactagtcg gcggccgctc tagagtatcc ctcgaggggc ccaagcttac gcgtacccag 300
ctttcttgtt caaaagtggtc cctatagtga gtctgttatt aagctaggca ctggccgtcg 360
ttttacaacg tcgtgactgg gaaaaactgct agcttggat ctttg 405

<210> 284
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<220>

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<220>

<221> CDS

<222> (31)..(153)

<223>

<400> 284

cggataacaa tttcacacag gaaaacagacc atg tcg tac tac cat cac cat cac
Met Ser Tyr Tyr His His His His His His 54
1 5

cat cac ggc atc aca agt ttg tac aaa aaa gca ggc ttt gaa aac ctg
His His Gly Ile Thr Ser Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu
10 15 20 102

tat ttt caa gga acc atg gag aaa aaa atc act gga tat acc acc gtt
Tyr Phe Gln Gly Thr Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val
25 30 35 40 150

gat
Asp 153

<210> 285

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> His6-CAT

<400> 285

Met Ser Tyr Tyr His His His His His His Gly Ile Thr Ser Leu Tyr
1 5 10 15

Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met Glu Lys
20 25 30

Lys Ile Thr Gly Tyr Thr Thr Val Asp
35 40